

## A REVIEW ON DROUGHT STRESS IN *SORGHUM BICOLOR*: PHYSIOLOGICAL AND MOLECULAR APPROACH

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**Abstract:** *Sorghum bicolor* is one of the diverse and staple food crops grown on earth. About 41.97 million hectares on the earth has been cultivated sorghum in the year of 2021-2022. Drought is prevailing problem and important factor all over the world on agriculture production. Along with that, climate change making a serious situation for the cultivation of crops. Sorghum is one of the excellent crops capable of adapting to drastic environmental changes. By understanding the mechanism behind the adaptation and tolerance to the drought, we can make better crop. This review covers the possible approaches in the drought tolerance of the Sorghum such as the morphological character determining the drought stress tolerances, microbial interactions forming symbionts and helping in stress tolerance, breeding and molecular approaches to improve the abiotic stress tolerance and the use of QTLs and Marker Assisted Selection for improving the drought tolerance.

**Keywords:** Drought stress, Tolerance, Drought genes, Breeding, QTLs

### INTRODUCTION

**S**orghum (*Sorghum bicolor*) commonly referred as Indian millet, is a cereal plant of the family Poaceae. The origin of the plant is considered to be Africa. It is a drought tolerant C<sub>4</sub> grass plant used for production of grains, forage, sugar, lignocellulosic biomass and a genetic model for C<sub>4</sub> grasses due to its relatively small genome (approximately 800 Mbp), diploid genetics, diverse germplasm and colinearity with other C<sub>4</sub> grass genomes (McCormick *et al.*, 2018). Sorghum is one of the staple food for many peoples of Africa and some parts of Asia. Products such as breads, cakes, porridge and alcoholic drink beer is made out of sorghum grains. Nearly all sorghum production (97%) in western hemisphere is for livestock feed and forage because it is a lower cost alternative to maize and requires less water to grow (Hancock, 2000). The growth stage of the crop and the environmental factors decides the water requirement for sorghum. As imbibitions is the first step of seed germination, water plays a critical role in it. Drought stress is a condition where water loss in plants exceeds the ability of plant roots to absorb water from soil, thereby affecting the plant metabolism and ultimately resulting in yield loss. Plants use three main strategies (drought escape, drought avoidance and drought tolerance) to survive under drought stress (Osmolovskaya *et al.*, 2018). Plants are adapter to tolerance by wide range of responses at physiological, molecular and biochemical levels. Sorghum can tolerate short period of less severe water deficit. However, long term and several stress can affect sorghum growth

and the final yield (Assefa *et al.*, 2010). It's tolerance to drought is a consequence of heritable morphological and anatomical characters (such as thick leaf wax and deep root system), physiological responses (such as osmotic adjustment and stay green trait) and adaptive mechanisms that allow tolerance under extreme drought conditions (Tari *et al.*, 2017). This review paper discusses about the drought stress and the physiological and molecular mechanisms in tolerating the drought stress and molecular methods of improving drought tolerance in sorghum.

#### Sorghum as a dry land crop

Sorghum is an important crop plant in Dry land agriculture. Sorghum's heat and drought tolerance make it well suited to the area's semi-arid summer growing conditions, and its genetic diversity makes the crop potentially useful as a forage, a gluten free grain source, and in biofuel production (Dahlberg *et al.*, 2011). Despite the level of environmental adaption that sorghum display, failure of seedling establishment due to abiotic stress is a major problem (Howarth *et al.*, 1996). One strategy for maintaining adequate moisture in the seed and root zone for a longer time period is deeper sowing of the seed, but in this case, growth depends longer on seed reserves before emergence occurs (Howarth *et al.*, 1996). Yield instability is another problem when growing grain sorghum in dryland regions. More consistent yields resulted in Australia when every third row or two row of every four rows were left blank compared with uniformly spaced 1-m rows when yields were 2500 kg ha<sup>-1</sup> or less (Bandura *et al.*, 2006). Drought stress affects starch synthesis and energy (ATP) production process through increased respiration

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rate, resulting in reduced index of seedling vigor, GRI and PG (Queiroz *et al.*, 2019). However, the effect of drought stress on different sorghum genotypes may differ due to the variability in their response to the stress. For example, drought stress during terminal post-flowering stage, genotypes with a high growth rate and short duration of grain filling produced larger grains compared to genotypes with longer duration of grain development (Tuinstraet *et al.*, 1997). Ngaraet *et al.*, (2021) reported that Plant response to drought stress and drought tolerance is a result of complex biological processes involving physiological, biochemical, genomic, proteomic and metabolomics changes.

#### **Morphological characters and adaptations of plants in drought stress**

Drought tolerance is the ability of a plant to endure the water deficit conditions. Most of the plants at their habitat has one or more adaptations to withstand stress conditions. Crops like sorghum are naturally adapted to dry conditions, while many crops like rice, wheat, maize are designed to adapt to drought conditions by either conventional breeding or through biotechnological approaches. Many structural adaptations like stomatal opening and closing, reduced number of leaf and leaf area, root system changes to increase water absorption, presence of small hairs called trichomes on leaf to absorb water from atmosphere. Plants growing in dry areas have developed xeromorphic traits to reduce transpiration under drought stress (Basuet *et al.*, 2016). Assefa (2012), reported that leaf rolling is a good indicator of drought tolerance in plants. Studies of Bibi *et al.*, (2012) reported that root length is an important trait against drought stress in plant varieties. The variety with longer root has the drought resistance ability to absorb nutrients and water availability in soil. Drought tolerance was found to be highly associated with root characteristics such as root thickness, root length density, number of thick roots, root volume and root dry weight (Wagaw, 2019). Many plants have modified leaf like pine needle and avoid drought through sunken stomata. Sorghum and wheat have waxy covering of plant cuticle to control transpiration. This trait was found to be associated with seedling stage of drought tolerance in sorghum.

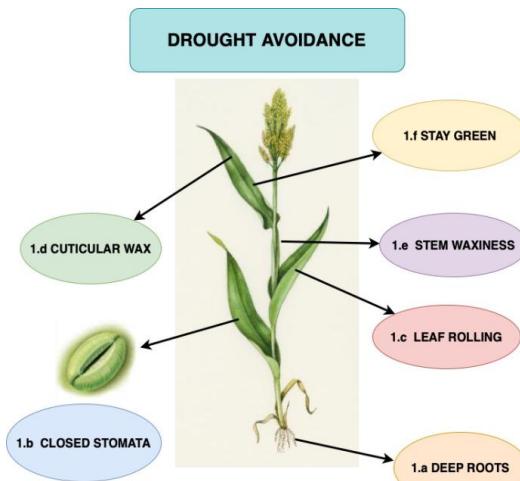
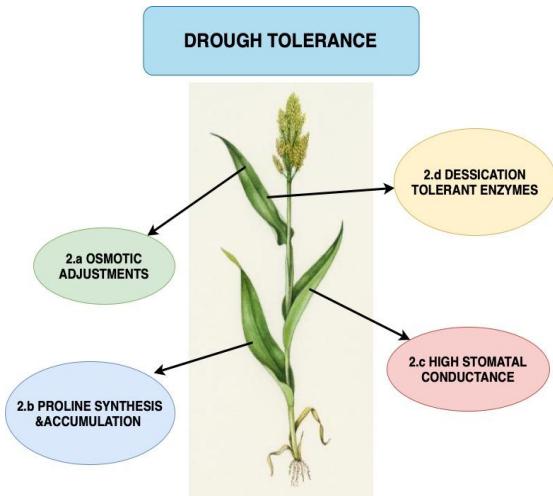
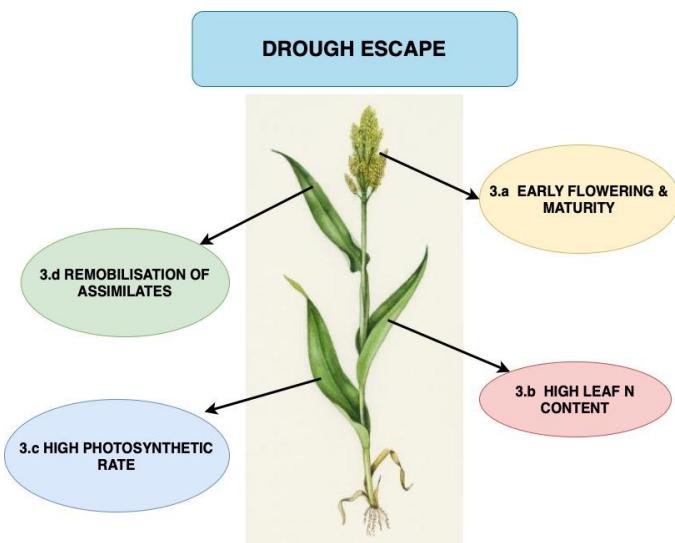
#### **Symbionts based approach to abiotic stress**

Microbial interactions with crop plants are key to the adaptation and survival of both the partners in any abiotic environment. Induced Systemic Tolerance (IST) is the term being used for microbe-mediated induction of abiotic stress responses (Meena *et al.*,

2017). Plant growth promoting microbes (Symbionts) are capable of conferring stress tolerance to various host plants and beneficiary to both monocot and dicot crop species. Marasco *et al.*, (2013) reported that microbes isolated from the roots of one host species cultivated under dessert farming conditions are capable of improving the growth of a different host species when grown under water-stress regime. Mayaket *et al.*, (2004), found that the bacterium *Achromobacter piechaudii*, isolated from dry riverbeds of southern Israel, was capable of increasing salt and drought resistance in both pepper and tomato. The Kapoor *et al.*, (2013) stated that Arbuscular Mycorrhizae enhance plant growth productivity and nutrient uptake under stress condition and also enhance osmolyte production, influence plant-water relation and rate of photosynthesis, alter leaf water potential, ionic balance, antioxidant production and other physiological and biological parameters and thus improve plant's capacity to tolerate abiotic stress. The findings of Symancziket *et al.*, (2018) suggested that under the drought stress condition, *Rhizophagusarabicus* transfers significantly more Nitrogen to sorghum than *Rhizophagusirregularis*. Recently, bacterial cold-shock proteins transformed into various plant species led to increased tolerance to a variety of abiotic stresses, including cold, heat, and drought (Castiglioni *et al.*, 2008).

#### **Breeding and molecular strategies for drought stress**

There are three mechanisms through which plants can survive drought tolerance. They are drought avoidance, (fig.1) drought tolerance (fig.2) and drought escape (fig.3). Understanding the genes involved in these mechanism help us to improve the plants to resist the drought and improve productivity. Sorghum is a short day plant, flowering initiation occur in 15<sup>th</sup> day when plants are exposed to short day light (10 hours) for 5 days (Caddel, 1972). Several salt, drought, and cold-tolerant lines have been developed through breeding and are being maintained in different locations all over the world (Maqbool *et al.*, 2001). In general, for self-pollinated crops, pedigree and bulk method can be used and for cross pollinated crops, recurrent selection can be used. Backcross could be used if drought resistant traits are transferring to a high yielding genotype. Biparental mating (half-sib & full sib) maintains the broad genetic base as well as provides the scope to evolve the desired genotype of drought resistance (Yunus *et al.*, 1982).

**Fig. 1.** Drought avoidance mechanisms**Fig. 2.** Drought tolerance mechanisms**Fig. 3.** Mechanisms associated with drought escape.

Identification of the molecular markers associated with yield or other morphological traits related to drought resistance, those markers could be used as selection criteria for drought resistance (Belete, 2018). Molecular markers linked to QTL for drought tolerance could be used in increasing efficiency of breeding efforts to select sorghum germplasm with enhanced drought tolerance once these markers are identified through carefully monitored characterization of appropriate germplasm under stress condition (Belete, 2018). Other techniques include biotechnological approach *ie.*, Introducing and expressing the drought tolerant gene to sorghum, which protect sorghum from drought stress. Gene transfer is efficient and time saving method compared to breeding method, which is highly suggestible in recent researches. Proline is an amino acid, which act as osmolytes in plants that protect plant from osmotic stress (Yoshiba *et al.*, 1997). *P5CSF129A* gene which synthesis mutated pyrroline 5-carboxylate synthetase, the key enzyme for proline biosynthesis from glutamic acid were transferred to

*Sorghum bicolor* through *Agrobacterium tumefaciens* mediated gene transfer and overexpressed. Proline accumulated in transgenic sorghum (Reddy, 2015 & Kishor, 1995). Transferring *mtlD* gene from *E. coli* into *Sorghum bicolor* which encodes for mannitol-1-phosphate dehydrogenase enzyme, as a result the crop can tolerate water deficit conditions (Maheswarie *et al.*, 2010). Mainly two approaches *ie.*, targeted and shotgun approach facilitate genetic engineering to obtain transgenic plants conferring drought resistance (Belete, 2018).

#### Genes associated with drought tolerance in sorghum

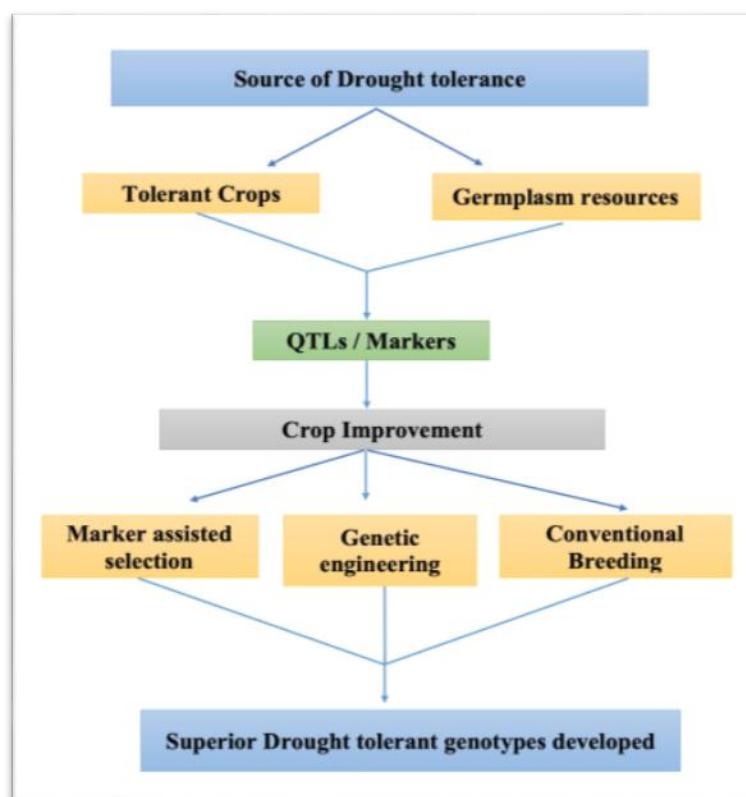
Cuticle is covered by a layer of wax called epicuticular wax. This wax is chemically made up of hydrophobic long chain organic compounds. This plays an chief role in controlling the cuticular transpiration. Many research have shown that drought stress can increase the amount of wax deposition on leaf surface (Yang *et al.*, 2011). Bao *et al* (2017) cloned the *SbWINL1* gene into *Arabidopsis*. The results revealed that overexpression

of SbWINL1 in *Arabidopsis* showed increase in wax and cutin. It was also reported that WIN1 gene is responsible for drought and defence responses in plants (Sela *et al.*, 2013). Li *et al* (2019) worked on *SbER1* and *SbER2*, genes that confer drought tolerance in maize. Their results proved that *SbER2-1* had an important role in drought stress. *SbSNAC1* is a plant specific NAC TF. This has a role in governing abiotic stress responses in sorghum. In response to ABA, *SbSNAC1* is found to have high expression rate in roots. Findings of Lu *et al* (2013) showed that overexpression of *SbSNAC1* gene in transgenic plants showed improved drought stress tolerance. Mittal *et al* (2017) concluded that many drought responsive CDPKs were associated with regulation to confer drought tolerance. Expression of *SbWRKY30* gene promises drought tolerance in *Arabidopsis*. Thus *SbWRKY30* may be a candidate gene for drought tolerance (Yang *et al.*, 2020).

#### QTLs and Marker Assisted Selection for drought tolerance breeding

Quantitative Trait Locus (QTL) is the method of locating the genes for quantitative traits with the help of molecular markers. There are many traits identified that govern drought tolerance and are been mapped on sorghum genome. Tunisraet *et al.*, (1997) studied a set of 98 recombinant inbred sorghum lines

for post flowering drought tolerance through QTL. The overview of breeding approach for drought tolerance is given in fig.1. Stay – green in sorghum is one among the very needed trait for drought tolerance. Stay – green trait is the ability of sorghum plant to retain the green leaves even under physiological stress that can enhance the photosynthetic rate. Marker Assisted Selection helps in selection of the parental genotype with the contrasting traits for crop improvement. Molecular markers includes RFLP, RAPD, SSR, AFLP, SNP etc. Among these, Single Nucleotide Polymorphism (SNP) markers can detect the diversity at a single base level (Disasaet *et al.*, 2016). The SSR markers were found to ease the transfer of important stay-green QTL to sorghum cultivars of interest (Edema and Amoding, 2015). Abou-Elwafa and Shehzad (2018) studied the molecular diversity among 96 sorghum lines with molecular markers. They reported their findings of three drought responsive QTLs ie., *Xtp69* on chromosome 3, *SbAGA01* on chromosome 8 and *SbAGB03* on chromosome 9. these genes are associated with drought resistant linked phenotypic traits. A collective breeding approaches can be screened and used to develop drought tolerant superior cultivars.



**Fig. 1.** An overview of collective methods of crop improvement for drought stress

#### CONCLUSION

Water is one among the basic necessities to maintain life processes. Ultimately irrigation for crops is

essential for food security on a global level. Climate changes in the present world contributes majorly for the abiotic stress in plants. Drought stress is normally considered to create a negative impact on plant

growth and yield. Generally, plants adopt themselves to survive in stress conditions. Severe drought can result in disturbing the photosynthetic rate, leading to altered plant metabolism and thereby resulting in crop failure and yield loss. In the view of crop improvement, understanding the principles of physiological and molecular basis of drought stress is required. Sorghum is naturally referred as camel crop as it is having the high ability of drought tolerance and thus performs well. It is also a C4 plant of good photosynthesis efficiency. Drought stress affects sorghum at every growth stages. So, to gain more understanding of stress effect on plants, detailed molecular study must be done at specific growth stages. Further research should be done on studying the combined abiotic stress components in sorghum for crop improvement. In regard to this, screening for new genotypes with high drought tolerance should be done. Many drought stress governing genes have been mapped and few were also discussed above and molecular mechanisms associated with that are also found. Finally to conclude, the advances that proceed in genetic and molecular studies and modern breeding strategies will enhance sorghum in conferring high degrees of stress tolerance.

## REFERENCES

**Abou-Elwafa, S.F. and Shehzad, T.** (2018). Genetic identification and expression profiling of drought responsive genes in sorghum. *Environ. Exp. Bot.* 155, 12 – 20. [Google Scholar](#)

**Assefa, Amelework Beyene** (2012). Genetic diversity analysis of lowland sorghum [*Sorghum bicolor* (L.) Moench] landraces under moisture stress conditions and breeding for drought tolerance in North Eastern Ethiopia (Doctoral dissertation, UNIVERSITY OF KWAZULU-NATA). [Google Scholar](#)

**Assefa, Y., Staggenborg, S. A. and Prasad, V. P. V.** (2010). Grain sorghum water requirement and responses to drought stress: A review. *Online. Crop Management* doi:10.1094/CM-2010-1109-01-RV. [Google Scholar](#)

**Bandaru, V., Stewart, B. A., Baumhardt, R. L., Ambati, S., Robinson, C. A. and Schlegel, A.** (2006). Growing dryland grain sorghum in clumps to reduce vegetative growth and increase yield. *Agronomy Journal*, 98(4), 1109-1120. [Google Scholar](#)

**Basu, S., Ramegowda, V., Kumar, A. and Pereira, A.** (2016). Plant adaptation to drought stress. *F1000Research*, 5, F1000 Faculty Rev-1554. [Google Scholar](#)

**Bao, S.G., Shi, J.X., Luo, F., Ding, B., Hao, J., Xie, X.D. and Sun, S.** (2017). Overexpression of Sorghum *WINL1* gene confers drought tolerance in *Arabidopsis thaliana* through the regulation of cuticular biosynthesis. *Plant Cell Tiss Organ Cult* 128, 347–356. [Google Scholar](#)

**Belete, T.** (2018). Breeding for resistance to drought: A case in sorghum (*Sorghum bicolor* (L.) Moench). *J Agric Forest Meteorol Res*, 1(1), 1-10. [Google Scholar](#)

**Bibi, A., Sadaqat, H. A., Tahir, M. H. N. and Akram, H. M.** (2012). Screening of sorghum (*Sorghum bicolor* var Moench) for drought tolerance at seedling stage in polyethylene glycol. *J. Anim. Plant Sci*, 22(3), 671-678. [Google Scholar](#)

**Caddel, J. L. and Weibel, D. E** (1972). Photoperiodism in Sorghum 1. *Agronomy Journal*, 64(4), 473-476. [Google Scholar](#)

**Castiglioni, P., Warner, D., Bensen, R. J., Anstrom, D. C., Harrison, J., Stoecker, M. and Heard, J. E** (2008). Bacterial RNA chaperones confer abiotic stress tolerance in plants and improved grain yield in maize under water-limited conditions. *Plant physiology*, 147(2), 446-455. [Google Scholar](#)

**Dahlberg, J., Berenji, J., Sikora, V. and Latkovic, D.** (2012). Assessing sorghum [*Sorghum bicolor* (L.) Moench] germplasm for new traits: food, fuels & unique uses. *Maydica*, 56(2). [Google Scholar](#)

**Disasa, T., Feyissa, T., Admassu, B., Paliwal, R., Villiers, S.D. and Odony, D.A.** (2016). Molecular evaluation of Ethiopian sweet sorghum germplasm and their contribution to regional breeding programs. *Aust. J. Crop Sci*, 10, 520 – 527. [Google Scholar](#)

**Edema, R. and Amoding, G.K.** (2015). Validating Simple Sequence Repeats (SSR) markers for introgression of stay-green Quantitative Trait Loci (QTL) into elite sorghum lines. *Afr. J. Biotechnol.* 14(46), 3101 – 3111. [Google Scholar](#)

**Hancock, J.D.** (2000). “Value of sorghum and sorghum co-products in diets for livestock”, in: Smith, C.W. and R.A. Frederiksen (eds.), *Sorghum: Origin, History, Technology, and Production*, John Wiley & Sons, New York, 731-749. [Google Scholar](#)

**Howarth, C. J., Rattunde, E. W., Bidinger, F. R. and Harris, D.** (1996). Seedling survival of abiotic stress: Sorghum and pearl millet. [Google Scholar](#)

**Kapoor, R., Evelin, H., Mathur, P. and Giri, B.** (2013). Arbuscular mycorrhiza: approaches for abiotic stress tolerance in crop plants for sustainable agriculture. In *Plant acclimation to environmental stress* (pp. 359-401). Springer, New York, NY. [Google Scholar](#)

**Kishor, P. K., Hong, Z., Miao, G. H., Hu, C. A. A. and Verma, D. P. S.** (1995). Overexpression of [delta]-pyrroline-5-carboxylate synthetase increases

proline production and confers osmotolerance in transgenic plants. *Plant physiology*, 108(4), 1387-1394.

[Google Scholar](#)

**Li, H., Han, X., Liu, X., Zhou, M., Ren, W., Zhao, B., Ju, C., Liu, Y. and Zhao, J.** (2019). A leucine-rich repeat-receptor-like kinase gene SbER2-1 from sorghum (*Sorghum bicolor L.*) confers drought tolerance in maize. *BMC genomics*, 20(1), 737.

[Google Scholar](#)

**Lu, M., Zhang, DF., Shi, YS. et al.** Expression of *SbSNAC1*, a NAC transcription factor from sorghum, confers drought tolerance to transgenic *Arabidopsis*. *Plant Cell Tiss Organ Cult* 115, 443–455 (2013).

[Google Scholar](#)

**Maheswari, M., Varalaxmi, Y., Vijayalakshmi, A., Yadav, S. K., Sharmila, P., Venkateswarlu, B. and Saradhi, P. P.** (2010). Metabolic engineering using mtID gene enhances tolerance to water deficit and salinity in sorghum. *Biologia Plantarum*, 54(4), 647-652.

[Google Scholar](#)

**Maqbool, S. B., Devi, P. and Sticklen, M. B.** (2001). Biotechnology: Genetic improvement of sorghum (*Sorghum bicolor (L.) Moench*). *In Vitro Cellular & Developmental Biology-Plant*, 37(5), 504-515.

[Google Scholar](#)

**Marasco, R., Rolli, E., Vigani, G., Borin, S., Sorlini, C., Ouzari, H. and Daffonchio, D.** (2013). Are drought-resistance promoting bacteria cross-compatible with different plant models?. *Plant signaling & behavior*, 8(10), e26741.

[Google Scholar](#)

**Mayak, S., Tirosh, T. and Glick, B. R.** (2004). Plant growth-promoting bacteria confer resistance in tomato plants to salt stress. *Plant physiology and Biochemistry*, 42(6), 565-572.

[Google Scholar](#)

**McCormick, R. F., Truong, S. K., Sreedasyam, A., Jenkins, J., Shu, S., Sims, D., Kennedy, M., Amirebrahimi, M., Weers, B. D., McKinley, B., Mattison, A., Morishige, D. T., Grimwood, J., Schmutz, J. and Mullet, J. E** (2018). The *Sorghum bicolor* reference genome: improved assembly, gene annotations, a transcriptome atlas, and signatures of genome organization. *The Plant journal : for cell and molecular biology*, 93(2), 338–354.

[Google Scholar](#)

**Meena, K. K., Sorty, A. M., Bitla, U. M., Choudhary, K., Gupta, P., Pareek, A. and Minhas, P. S.** (2017). Abiotic stress responses and microbe-mediated mitigation in plants: the omics strategies. *Frontiers in plant science*, 8, 172.

[Google Scholar](#)

**Mittal, S., Mallikarjuna, M. G., Rao, A. R., Jain, P. A., Dash, P. K. and Thirunavukkarasu, N.** (2017). Comparative analysis of CDPK family in maize, *Arabidopsis*, rice, and sorghum revealed

potential targets for drought tolerance improvement. *Frontiers in Chemistry*, 5, 115.

[Google Scholar](#)

**Ngara, R., Goche, T., Swanevelder, D. Z. and Chivasa, S.** (2021). Sorghum's Whole-Plant Transcriptome and Proteome Responses to Drought Stress: A Review. *Life*, 11(7), 704.

[Google Scholar](#)

**Osmolovskaya N., Shumilina J., Kim A., Didio A., Grishina T., Bilova T., Keltsieva O.A., Zhukov V., Tikhonovich I., Tarakhovskaya E., et al.** Methodology of Drought Stress Research: Experimental Setup and Physiological Characterization. *Int. J. Mol. Sci.* 2018;19:4089.

[Google Scholar](#)

**Queiroz, M. S., Oliveira, C. E., Steiner, F., Zuffo, A. M., Zoz, T., Vendruscolo, E. P. and Menis, F. T.** (2019). Drought stresses on seed germination and early growth of maize and sorghum. *Journal of Agricultural Science*, 11(2), 310-318.

[Google Scholar](#)

**Reddy, P. S., Jogeswar, G., Rasineni, G. K., Maheswari, M., Reddy, A. R., Varshney, R. K. and Kishor, P. K.** (2015). Proline over-accumulation alleviates salt stress and protects photosynthetic and antioxidant enzyme activities in transgenic sorghum [*Sorghum bicolor (L.) Moench*]. *Plant Physiology and Biochemistry*, 94, 104-113.

[Google Scholar](#)

**Sela, D., Buxdorf, K., Shi, J. X., Feldmesser, E., Schreiber, L., Aharoni, A. and Levy, M.** (2013). Overexpression of SHN1/WIN1 provokes unique defense responses. *PloS one*, 8(7), e70146.

[Google Scholar](#)

**Symanczik, S., Lehmann, M. F., Wiemken, A., Boller, T. and Courty, P. E** (2018). Effects of two contrasted arbuscular mycorrhizal fungal isolates on nutrient uptake by *Sorghum bicolor* under drought. *Mycorrhiza*, 28(8), 779-785.

[Google Scholar](#)

**Tari L, Laskay G., Takács Z., Poór P.** Response of Sorghum to Abiotic Stresses: A Review. *J. Agron. Crop Sci.* 2013;199:264–274.

[Google Scholar](#)

**Tuinstra, M. R., Grote, E. M., Goldsbrough, P. B. and Ejeta, G.** (1997). Genetic analysis of post-flowering drought tolerance and components of grain development in *Sorghum bicolor (L.) Moench*. *Mol. Breed.*, 3(6), 439-448.

[Google Scholar](#)

**Wagaw, K.** (2019). Review on Mechanisms of Drought Tolerance in Sorghum (*Sorghum bicolor L.* Moench) Basis and Breeding Methods. *Academic Research Journal of Agricultural Science and Research*.7(2), 87-99.

[Google Scholar](#)

**Yang, J., Ordiz, M. L., Jaworski, J. G. and Beachy, R. N.** (2011). Induced accumulation of cuticular waxes enhances drought tolerance in

Arabidopsis by changes in development of stomata. *Plant Physiology and Biochemistry*, 49(12), 1448-1455.

[Google Scholar](#)

Yang, Z., Chi, X., Guo, F., Jin, X., Luo, H., Hawar, A., Chen, Y., Feng, K., Wang, B., Qi, J., Yang, Y. and Sun, B. (2020). *SbWRKY30* enhances the drought tolerance of plants and regulates a drought stress-responsive gene, *SbRD19*, in sorghum. *Journal of plant physiology*, 246-247, 153142.

[Google Scholar](#)

Yoshiba, Y., Kiyosue, T., Nakashima, K., Yamaguchi-Shinozaki, K. and Shinozaki, K. (1997). Regulation of levels of proline as an osmolyte in plants under water stress. *Plant and Cell Physiology*, 38(10), 1095-1102.

[Google Scholar](#)

Yunus, M. and Paroda, R. S. (1982). Impact of biparental mating on correlation coefficients in bread wheat. *Theoretical and Applied Genetics*, 62(4), 337-343.

[Google Scholar](#)

